

WO 01/17334

PCT/NZ00/00176

SEQUENCE LISTING

<110> The Horticulture and Food Research Institute of NZ

<120> Seedless Fruit Production

<130> 26329 MRB

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<150> NZ337688

<151> 1999-09-07

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 868

<212> DNA

<213> Malus domestica

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<221> CDS

<222> (1)..(648)

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Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Ile Lys Lys Ala

20 25 30

aag gag atc act gtt cta tgt gat gct aaa gta tct ctt atc att tat 144

Lys Glu Ile Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Ile Tyr

35 40 45

tct agc tct ggg aag atg gtt gaa tac tgc agc cct tca act acg ctg 192

Ser Ser Ser Gly Lys Met Val Glu Tyr Cys Ser Pro Ser Thr Thr Leu

50 55 60

aca gaa atc ttg gac aaa tac cat gga caa tct ggg aag aag ttg tgg 240

Thr Glu Ile Leu Asp Lys Tyr His Gly Gln Ser Gly Lys Lys Leu Trp

65 70 75 80

gat gct aag cat gag aac ctc agc aat gaa gtg gat aga gtc aag aaa 288
Asp Ala Lys His Glu Asn Leu Ser Asn Glu Val Asp Arg Val Lys Lys
85 90 95

gac aat gac agc atg caa gta gag ctc agg cat ctg aag gga gag gat 336
Asp Asn Asp Ser Met Gln Val Glu Leu Arg His Leu Lys Gly Glu Asp
100 105 110

atc aca tca ttg aac cat gta gag ctg atg gcc tta gag gaa gca ctt 384
Ile Thr Ser Leu Asn His Val Glu Leu Met Ala Leu Glu Glu Ala Leu
115 120 125

gaa aat ggc ctt aca agt atc cgg gac aag cag tcc aag ttc gtc gac 432
Glu Asn Gly Leu Thr Ser Ile Arg Asp Lys Gln Ser Lys Phe Val Asp
130 135 140

atg atg aga gac aat gga aag gca ctg gaa gat gag aat aag cgc ctc 480
Met Met Arg Asp Asn Gly Lys Ala Leu Glu Asp Glu Asn Lys Arg Leu
145 150 155 160

act tat gag ctg caa aaa caa cag gag atg aaa ata aaa gag aat gtg 528
Thr Tyr Glu Leu Gln Lys Gln Gln Glu Met Lys Ile Lys Glu Asn Val
165 170 175

aga aac atg gaa aat ggg tat cat cag agg cag ctg ggg aac tac aac 576
Arg Asn Met Glu Asn Gly Tyr His Gln Arg Gln Leu Gly Asn Tyr Asn
180 185 190

aac aac cag cag cag ata cct ttt gcc ttc cgc gtg cag cct att cag 624
Asn Asn Gln Gln Gln Ile Pro Phe Ala Phe Arg Val Gln Pro Ile Gln
195 200 205

cca aat ctc cag gag aga atc taa ttagatatat cttgcatttg catgctcttt 678
Pro Asn Leu Gln Glu Arg Ile
210 215

ctaactagtt atattatctc tccacctctc tctctctttt catctgtcaa ggagttctta 738

agtttatgtc agatttccaa tggtttgtaa tggaattagc ttcgttatga ggctttgttg 798

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<213> Malus domestica

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Lys Glu Ile Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Ile Tyr
      35           40           45
Ser Ser Ser Gly Lys Met Val Glu Tyr Cys Ser Pro Ser Thr Thr Leu
 50           55           60
Thr Glu Ile Leu Asp Lys Tyr His Gly Gln Ser Gly Lys Lys Leu Trp
 65           70           75           80
Asp Ala Lys His Glu Asn Leu Ser Asn Glu Val Asp Arg Val Lys Lys
      85           90           95
Asp Asn Asp Ser Met Gln Val Glu Leu Arg His Leu Lys Gly Glu Asp
      100          105          110
Ile Thr Ser Leu Asn His Val Glu Leu Met Ala Leu Glu Glu Ala Leu
      115          120          125
Glu Asn Gly Leu Thr Ser Ile Arg Asp Lys Gln Ser Lys Phe Val Asp
      130          135          140
Met Met Arg Asp Asn Gly Lys Ala Leu Glu Asp Glu Asn Lys Arg Leu
      145          150          155          160
Thr Tyr Glu Leu Gln Lys Gln Gln Glu Met Lys Ile Lys Glu Asn Val
      165          170          175
Arg Asn Met Glu Asn Gly Tyr His Gln Arg Gln Leu Gly Asn Tyr Asn
      180          185          190
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 1           5           10           15

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Gln Glu Leu Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Met Leu	
35 40 45	
tcc aac act aat aaa atg cac gag tat atc agc cct acc act acg acc	192
Ser Asn Thr Asn Lys Met His Glu Tyr Ile Ser Pro Thr Thr Thr Thr	
50 55 60	
aag agt atg tat gat gac tat cag aaa act atg ggg atc gat ctg tgg	240
Lys Ser Met Tyr Asp Asp Tyr Gln Lys Thr Met Gly Ile Asp Leu Trp	
65 70 75 80	
agg aca cac gag gag tcg atg aaa gac acc ttg tgg aag ttg aaa gag	288
Arg Thr His Glu Glu Ser Met Lys Asp Thr Leu Trp Lys Leu Lys Glu	
85 90 95	
atc aac aat aag ctg agg aga gag atc agg cag agg ttg ggc cat gat	336
Ile Asn Asn Lys Leu Arg Arg Glu Ile Arg Gln Arg Leu Gly His Asp	
100 105 110	
cta aat ggc ctg agc ttt gac gag ctg gct tct ctt gac gat gag atg	384
Leu Asn Gly Leu Ser Phe Asp Glu Leu Ala Ser Leu Asp Asp Glu Met	
115 120 125	
cag tct tcc ttg gat gcc ata cgt caa agg aag tac cat gtg atc aaa	432
Gln Ser Ser Leu Asp Ala Ile Arg Gln Arg Lys Tyr His Val Ile Lys	
130 135 140	
act cag acg gag acc acc aag aag aag gtt aag aac ttg gag caa aga	480
Thr Gln Thr Glu Thr Thr Lys Lys Lys Val Lys Asn Leu Glu Gln Arg	
145 150 155 160	
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Arg Gly Asn Met Leu His Gly Tyr Phe Asp Gln Glu Ala Ala Gly Glu	
165 170 175	
gat cca cag tat ggt tat gag gac aat gag gga gac tac gaa tct gca	576
Asp Pro Gln Tyr Gly Tyr Glu Asp Asn Glu Gly Asp Tyr Glu Ser Ala	
180 185 190	
ctt gca ttg tca aat ggg gcg aat aac ttg tac act ttc cac ctc cac	624
Leu Ala Leu Ser Asn Gly Ala Asn Asn Leu Tyr Thr Phe His Leu His	
195 200 205	

cac cct aac ctg cac cac gga gga agc tcg ctc ggc tcc tcc att act 672
 His Pro Asn Leu His His Gly Gly Ser Ser Leu Gly Ser Ser Ile Thr
 210 215 220

cat ctg cac gat ctc cgc ctt gct tga tcgtgatctg agatatgatt 719
 His Leu His Asp Leu Arg Leu Ala
 225 230

aatcatcact aagttatata ttaagggtcac ttataactgc ttttgctcta aagtgtttgc 779

ttggtgacta tcttttaggca aggagttaga cttggactac ctctgaaaac agatgcataa 839

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<212> PRT

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 Gln Glu Leu Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Met Leu
 35 40 45
 Ser Asn Thr Asn Lys Met His Glu Tyr Ile Ser Pro Thr Thr Thr Thr
 50 55 60
 Lys Ser Met Tyr Asp Asp Tyr Gln Lys Thr Met Gly Ile Asp Leu Trp
 65 70 75 80
 Arg Thr His Glu Glu Ser Met Lys Asp Thr Leu Trp Lys Leu Lys Glu
 85 90 95
 Ile Asn Asn Lys Leu Arg Arg Glu Ile Arg Gln Arg Leu Gly His Asp
 100 105 110
 Leu Asn Gly Leu Ser Phe Asp Glu Leu Ala Ser Leu Asp Asp Glu Met
 115 120 125
 Gln Ser Ser Leu Asp Ala Ile Arg Gln Arg Lys Tyr His Val Ile Lys
 130 135 140
 Thr Gln Thr Glu Thr Thr Lys Lys Lys Val Lys Asn Leu Glu Gln Arg
 145 150 155 160
 Arg Gly Asn Met Leu His Gly Tyr Phe Asp Gln Glu Ala Ala Gly Glu
 165 170 175
 Asp Pro Gln Tyr Gly Tyr Glu Asp Asn Glu Gly Asp Tyr Glu Ser Ala

	180		185		190										
Leu	Ala	Leu	Ser	Asn	Gly	Ala	Asn	Asn	Leu	Tyr	Thr	Phe	His	Leu	His
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His	Pro	Asn	Leu	His	His	Gly	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Ile	Thr
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Made in lab

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